1648

RAW SEQUENCE LISTING   DATE: 06/06/2002
PATENT APPLICATION: US/09/855,754A   TIME: 12:32:52

Input Set : A:\03495206.txt
Output Set: N:\CRF3\06062002\I855754A.raw

Does Not Comply
Corrected Diskette Needed

```
 3 <110> APPLICANT: BOURSAUX-EUDE, CAROLINE
 4         GUISO-MACLOUF, NICOLE
 6 <120> TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
 7         REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
 8         BORDETELLA PARAPERTUSSIS, AND BORDETELLA
 9         BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
10         IMMUNOGENIC COMPOSITIONS
12 <130> FILE REFERENCE: 03495-0206-00000
14 <140> CURRENT APPLICATION NUMBER: 09/855,754A
15 <141> CURRENT FILING DATE: 2000-11-15
17 <150> PRIOR APPLICATION NUMBER: 60/206,969
18 <151> PRIOR FILING DATE: 2000-05-25
20 <160> NUMBER OF SEQ ID NOS: (24) 25
22 <170> SOFTWARE: PatentIn Ver. 2.1
```

E-->

ERRORED SEQUENCES

<210> 25 *last sequence in submitted file*
<211> 5
<212> PRT
<213> (Artificial) *see item 11 on Erra Summary Sheet*

<220>
<221> MISC_FEATURE
<222> (3)..(4)
<223> Xaa can be any amino acid

<400> 25
Gly Gly Xaa Xaa Pro
  1   5

VERIFICATION SUMMARY   DATE: 06/06/2002
PATENT APPLICATION: US/09/855,754A   TIME: 12:32:54

Input Set : **A:\03495206.txt**
Output Set: **N:\CRF3\06062002\I855754A.raw**

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1065 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:1073 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:20 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (24) Counted (25)

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/855,754A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial-Sequence

11 ✓____Use of <220>

Sequence(s) _25_ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.